

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: de Boer, Piet A.J.
Hale, Cynthia A.
- (ii) TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR SCREENING
ANTIMICROBIALS
- (iii) NUMBER OF SEQUENCES: 25
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: MEDLEN & CARROLL
 - (B) STREET: 220 Montgomery Street, Suite 2200
 - (C) CITY: San Francisco
 - (D) STATE: California
 - (E) COUNTRY: United States of America
 - (F) ZIP: 94104
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Carroll, Peter G.
 - (B) REGISTRATION NUMBER: 32,837
 - (C) REFERENCE/DOCKET NUMBER: CASE-02249
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (415) 705-8410
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2160 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAATACCAGG GATGAAGTAA AGAATTAGTA ATACAATTGC GCGCGGCAGA TACCAGGCAA	60
ATTTTGTCCA TTCGCGTTTC ATGATTCGCG GCACATCTTT CATGATACCG AAAATCCCGG	120
TATCTGGCGG TGTAGCGCCA GTCAATCGTG CTTCCAGTTG TTCAGCCAAT AAACCGTTAA	180
ACGGAGCGGC AATCCAGTTA GCAATCGTGG AGAAGAAATA GCCAAACACT AACAGCACAG	240
AGATGACACG CAGAGGCCAC AACAGATAAC TCAGCCATTG TAGCCAGTCC GGAACGTAAC	300

TCATGAGAGT	CGGGATCCAG	ACATCGAGCT	GTGTAAAGAG	CCACCAGAAT	GCGCCCCCA	360
TCAACAAAAT	ATTGACCAGC	AGCGGTAAAA	TAACGAAACG	CCGAATCCCA	GGTTGCGAGA	420
CGAGCTTCCA	GCCTTGCGCA	AAATAGTAAA	AACCGCTGCG	TGGGGCAGAT	GTGAATGATG	480
AAACCATAAT	CAGGATGAGC	TCCTTTTGAC	CAATCCCAGG	AAAATTCTGC	GTATTTTACC	540
GGGTAATTGC	GCAATGGACA	GTTAGGATAT	GTTCGAAAAA	ACAGCAAAAA	GCACGATTTC	600
ATCTATCTTT	GTGCTGTGAA	AGTTAATAGT	GCACTTGAC	TTGAGGTAAT	CGGCAAATAC	660
TCTTAGTGAG	TAAATGTTTG	CCGTGGTGGC	AAGGTGTTAG	AACAACAGAG	AATATAATGA	720
TGCAGGATTT	GCGTCTGATA	TTAATCATTG	TTGGCGCGAT	CGCCATAATC	GCTTTACTGG	780
TACATGGTTT	CTGGACCAGC	CGTAAAGAAC	GATCTTCTAT	GTTCCGCGAT	CGGCCATTAA	840
AACGAATGAA	GTCAAAACGT	GACGACGATT	CTTATGACGA	GGATGTCGAA	GATGATGAGG	900
GCGTTGGTGA	GGTTCGTGTT	CACCGCGTGA	ATCATGCCCC	GGCTAACGCT	CAGGAGCATG	960
AGGCTGCTCG	TCCGTCGCCG	CAACACCAGT	ACCAACCGCC	TTATGCGTCT	GCGCAGCCGC	1020
GTCAACCGGT	CCAGCAGCCG	CCTGAAGCGC	AGGTACCGCC	GCAACATGCT	CCGCATCCAG	1080
CGCAGCCGGT	GCAGCAGCCT	GCCTATCAGC	CGCAGCCTGA	ACAGCCGTTG	CAGCAGCCAG	1140
TTTCGCCACA	GGTCGCGCCA	GCGCCGCAGC	CTGTGCATTG	AGCACCGCAA	CCGGCACAAC	1200
AGGCTTTCCA	GCCTGCAGAA	CCCGTAGCGG	CACCACAGCC	TGAGCCTGTA	GCGGAACCTG	1260
CTCCAGTTAT	GGATAAACCG	AAGCGCAAAG	AAGCGGTGAT	TATCATGAAC	GTCGCGGCGC	1320
ATCACGGTAG	CGAGCTAAAC	GGTGAAGCTC	TTCTTAACAG	CATTCAACAA	GCGGGCTTCA	1380
TTTTTGCGGA	TATGAATATT	TACCATCGTC	ATCTTAGCCC	GGATGGCAGC	GGCCCGGCGT	1440
TATTCAGCCT	GGCGAATATG	GTGAAACCGG	GAACCTTTGA	TCCTGAAATG	AAGGATTTCA	1500
CTACTCCGGG	TGTCACTATC	TTTATGCAGG	TACCGTCTTA	CGGTGACGAG	CTGCAGAACT	1560
TCAAGCTGAT	GCTGCAATCT	GCGCAGCATA	TTGCCGATGA	AGTGGGCGGT	GTCGTGCTTG	1620
ACGATCAGCG	CCGTATGATG	ACTCCGCAGA	AATTGCGCGA	GTACCAGGAC	ATCATCCGCG	1680
AAGTCAAAGA	CGCCAACGCC	TGATACACTT	AAGGCAAATT	AACTCCTCTT	CGAACCCCCG	1740
CTTGTCGGGG	GTTTTTAGCA	TTGATGGTGC	GATATGGAAT	CAATCGAACA	ACAACTGACA	1800
GAACTGCGAA	CGACGCTTCG	CCATCATGAA	TATCTTTATC	ATGTGATGGA	TGCGCCGGAA	1860
ATTCCCAGCG	CTGAATACGA	CAGGCTGATG	CGCGAACTGC	GCGAGCTGGA	AACCAAACAT	1920
CCAGAACTGA	TTACGCCTGA	TTCGCCTACT	CAACGTGTAG	GCGCTGCGCC	GCTGGCGGCT	1980
TTCAGCCAGA	TACGCCATGA	AGTACCAATG	CTGTCACTGG	ATAACGTTTT	TGATGAAGAA	2040
AGCTTTCTTG	CTTTCAACAA	ACGTGTGCAG	GACCGTCTGA	AAAACAACGA	GAAAGTCACC	2100
TGGTGCTGTG	AGCTGAAGCT	GGATGGTCTT	GCCGTCAGTA	TTCTGTATGA	AAATGGCGTT	2160

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Met Gln Asp Leu Arg Leu Ile Leu Ile Ile Val Gly Ala Ile Ala
1 5 10 15
Ile Ile Ala Leu Leu Val His Gly Phe Trp Thr Ser Arg Lys Glu Arg
20 25 30
Ser Ser Met Phe Arg Asp Arg Pro Leu Lys Arg Met Lys Ser Lys Arg
35 40 45
Asp Asp Asp Ser Tyr Asp Glu Asp Val Glu Asp Asp Glu Gly Val Gly
50 55 60
Glu Val Arg Val His Arg Val Asn His Ala Pro Ala Asn Ala Gln Glu
65 70 75 80
His Glu Ala Ala Arg Pro Ser Pro Gln His Gln Tyr Gln Pro Pro Tyr
85 90 95
Ala Ser Ala Gln Pro Arg Gln Pro Val Gln Gln Pro Pro Glu Ala Gln
100 105 110
Val Pro Pro Gln His Ala Pro His Pro Ala Gln Pro Val Gln Gln Pro
115 120 125
Ala Tyr Gln Pro Gln Pro Glu Gln Pro Leu Gln Gln Pro Val Ser Pro
130 135 140
Gln Val Ala Pro Ala Pro Gln Pro Val His Ser Ala Pro Gln Pro Ala
145 150 155 160
Gln Gln Ala Phe Gln Pro Ala Glu Pro Val Ala Ala Pro Gln Pro Glu
165 170 175
Pro Val Ala Glu Pro Ala Pro Val Met Asp Lys Pro Lys Arg Lys Glu
180 185 190
Ala Val Ile Ile Met Asn Val Ala Ala His His Gly Ser Glu Leu Asn
195 200 205
Gly Glu Ala Leu Leu Asn Ser Ile Gln Gln Ala Gly Phe Ile Phe Gly
210 215 220
Asp Met Asn Ile Tyr His Arg His Leu Ser Pro Asp Gly Ser Gly Pro
225 230 235 240
Ala Leu Phe Ser Leu Ala Asn Met Val Lys Pro Gly Thr Phe Asp Pro
245 250 255
Glu Met Lys Asp Phe Thr Thr Pro Gly Val Thr Ile Phe Met Gln Val
260 265 270

Pro Ser Tyr Gly Asp Glu Leu Gln Asn Phe Lys Leu Met Leu Gln Ser
275 280 285

Ala Gln His Ile Ala Asp Glu Val Gly Gly Val Val Leu Asp Asp Gln
290 295 300

Arg Arg Met Met Thr Pro Gln Lys Leu Arg Glu Tyr Gln Asp Ile Ile
305 310 315 320

Arg Glu Val Lys Asp Ala Asn Ala
325

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 327 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Asp Leu Asn Thr Ile Leu Ile Ile Val Gly Ile Val Ala Leu Val Ala
1 5 10 15

Leu Ile Val His Gly Leu Trp Ser Asn Arg Arg Glu Lys Ser Lys Tyr
20 25 30

Phe Asp Lys Ala Asn Lys Phe Asp Arg Thr Ser Leu Thr Ser Arg Ser
35 40 45

His Thr Gln Glu Glu Met Val Gln Pro Asn Asn Ile Ser Pro Asn Thr
50 55 60

Tyr Val Glu Asn Gly His Thr Pro Ile Pro Gln Pro Thr Thr Glu Lys
65 70 75 80

Leu Pro Ser Glu Ala Glu Leu Ile Asp Tyr Arg Gln Ser Asp Lys Ser
85 90 95

Val Asp Asp Ile Lys Ile Ser Ile Pro Asn Thr Gln Pro Ile Tyr Asp
100 105 110

Met Gly Asn His Arg Ser Glu Pro Ile Gln Pro Thr Gln Pro Gln Tyr
115 120 125

Asp Met Pro Thr Ala Asn Asn Val Ala Ser Met Thr Leu Glu Gln Leu
130 135 140

Glu Ala Gln Ser Gln Asn Val Gly Phe Asn Gly Ile Asn Ser Ser Ser
145 150 155 160

Pro Glu Leu Arg Val Gln Leu Ala Glu Leu Ser His Glu Glu His Gln
165 170 175

Val Asp Tyr Asn Leu Ser Phe Asn Glu Pro Lys Ala Glu Thr Thr Ala
180 185 190

His Pro Lys Gln Thr Thr Gly Tyr Ile Gln Leu Tyr Leu Ile Pro Lys
195 200 205

Ser Ser Glu Glu Phe Asn Gly Ala Lys Leu Val Gln Ala Leu Glu Asn
 210 215 220
 Leu Gly Phe Ile Leu Gly Lys Asp Glu Met Tyr His Arg His Leu Asp
 225 230 235 240
 Leu Ser Val Ala Ser Pro Val Leu Phe Ser Val Ala Asn Leu Glu Gln
 245 250 255
 Pro Gly Thr Phe Asn Ala Tyr Asn Leu Ala Glu Phe Asn Thr Ile Gly
 260 265 270
 Ile Val Leu Phe Met Gln Leu Pro Ser Pro Gly Asn Asn Leu Ala Asn
 275 280 285
 Leu Arg Met Met Met Arg Ala Ala His Thr Leu Ala Glu Asp Leu Gln
 290 295 300
 Gly Val Ile Leu Thr Glu Glu Gln Glu Ile Phe Asp Ala Asn Ala Glu
 305 310 315 320
 Gln Ala Tyr Leu Ala Arg Val
 325

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ile Leu Ile Ile Val Gly
 1 5

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "The peptide at this location can be either Arg or Asn."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /note= "The peptide at this location can be either Leu or Thr."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asp Leu Xaa Xaa Ile Leu Ile Ile Val Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /note= "The peptide at this location can be either"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 8
- (D) OTHER INFORMATION: /note= "The peptide at this location can be either Ile or Val."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /note= "The peptide at this location can be either Ile or Leu."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /note= "The peptide at this location can be either Ile or Val."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ile Leu Ile Ile Val Gly Xaa Xaa Ala Xaa Xaa Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /note= "The peptide at this location can be either Ala or Leu."

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 8
 (D) OTHER INFORMATION: /note= "The peptide at this
location can be either Ile or Val."

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 10
 (D) OTHER INFORMATION: /note= "The peptide at this
location can be either Ile or Leu."

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 11
 (D) OTHER INFORMATION: /note= "The peptide at this
location can be either Ile or Val."

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 14
 (D) OTHER INFORMATION: /note= "The peptide at this
location can be either Ile or Leu."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ile Leu Ile Ile Val Gly Xaa Xaa Ala Xaa Xaa Ala Leu Xaa Val His
1 5 10 15

Gly

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 3
 (D) OTHER INFORMATION: /note= "The peptide at this
location can be either Ile or Leu."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ala Leu Xaa Val His Gly
1 5

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 3
 (D) OTHER INFORMATION: /note= "The peptide at this
location can be either Ile or Leu."

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 7
 (D) OTHER INFORMATION: /note= "The peptide at this
location can be either Phe or Leu."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ala Leu Xaa Val His Gly Xaa Trp
1 5

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Tyr His Arg His Leu
1 5

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 2
 (D) OTHER INFORMATION: /note= "The peptide at this
location can be either Ala or Val."

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 6
 (D) OTHER INFORMATION: /note= "The peptide at this
location can be either Leu or Val."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Pro Xaa Leu Phe Ser Xaa Ala Asn
1 5

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Pro Gly Thr Phe
1

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "The peptide at this location can be either Ile or Leu."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Xaa Phe Met Gln
1

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "The peptide at this location can be either Ile or Leu."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /note= "The peptide at this location can be either Val or Leu."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Xaa Phe Met Gln Xaa Pro Ser
1 5

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ACAGAGATCC ATATGATGCA GGATTTCGT CTG

33

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TTAACCAAGC TTAAGTGTAT CAGGCGTTGG

30

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AAGTCTCGAG GCGTTGGCG TCTTTGAC

28

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Leu Glu Asp Pro Pro Ala Glu Phe
1 5

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Gly His His His His His His His His His His Ser Ser Gly His
1 5 10 15
Ile Glu Gly Arg His Met Asp Tyr Lys Asp Asp Asp Asp Lys Ala Arg
20 25 30
Arg Ala Ser Val Glu Phe His Met Ala Ser Met Thr Gly Gly Gln Gln
35 40 45
Met Gly Arg Gly Ser
50

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Gly Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Gly His His His His His His His His His His Ser Ser Gly His
1 5 10 15
Ile Glu Gly Arg His
20

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met Asp Tyr Lys Asp Asp Asp Asp Lys Ala Arg Arg Ala Ser Val Glu
1 5 10 15
Phe

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met Gly His His His His His His His His His His Ser Ser Gly His
1 5 10 15
Ile Glu Gly Arg His Met Asp Tyr Lys Asp Asp Asp Asp Lys Ala Arg
20 25 30
Arg Ala Ser Val Glu Phe His Met Ala Ser Met Thr Gly Gly Gln Gln
35 40 45
Met Gly Arg Gly Ser His
50

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GGAGGATCCC ATATGTTTGA ACCAATGGAA C

31

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TTCCGGTCGA CTCTTAATCA GCTTGCTTAC G

31

TTCCGGTCGA CTCTTAATCA GCTTGCTTAC G